

VARIABLE HEAVY DOMAIN

		10	20	30	40
2C4	EVQLQQSGPELVKPGTSVKISKAS	[GFTFTDYTMD]	WVKQS		
	** ** *	* * * *	*	*	*
574	EVQLVESGGGLVQPGGSLRLSCAAS	[GFTFTDYTMD]	WVRQA		
		** *	*	*	*
hum III	EVQLVESGGGLVQPGGSLRLSCAAS	[GFTFSSYAMS]	WVRQA		

		50	a	60	70	80
2C4	HGKSLEWIG	[DVNPNSGGSIYNQRFKG]	KASLTVD	RSSRIVYM		
	* *	**	***	*	****	*
574	PGKGLEWVA	[DVNPNSGGSIYNQRFKG]	RFTLSVDRSKNTLYL			
		*****	***	****	*	*
hum III	PGKGLEWVA	[VISGDGGSTYYADSVKG]	RFTISRDN	SKNTLYL		

		abc	90	100ab	110
2C4	EIRSLTFE	TAVYYCAR	[NLGPSFYFDY]	WGQGT	TLTVSS
	***	**		**	
574	QMNSLRAED	TAVYYCAR	[NLGPSFYFDY]	WGQGT	TLTVSS

hum III	QMNSLRAED	TAVYYCAR	[GRVGYSLYDY]	WGQGT	TLTVSS

FIG. 1

Variable Light Domain

	10	20	30	40
2C4	DTVMTQSHKIMSTSVGDRVSITC	[KASQDVSIGVA]	WYQQRP	*
	**	**** *		
574	DIQMTQSPSSLASASVGDRVITIC	[KASQDVSIGVA]	WYQQKP	*
		* ** ***		
hum KI	DIQMTQSPSSLASASVGDRVITIC	[KASQDVSIGVA]	WYQQKP	
	50	60	70	80
2C4	GQSPKLLIY [SASYRYT]	GVPDRFTGSGSGTDFTFTISSVQA	*	*
	**	* *		
574	GKAPKLLIY [SASYRYT]	GVPSRFTGSGSGTDFTLTISLQ		
	* ****			
hum KI	GKAPKLLIY [AASSLES]	GVPSRFTGSGSGTDFTLTISLQ		
	90	100		
2C4	EDLAVYYC [QQYIYPYT]	FGGQKLEIKRT	*	*
	* *			
574	EDFATYYC [QQYIYPYT]	FGQGTKVEIKRT		
	*** *			
hum KI	EDFATYYC [QQYNSLPWT]	FGQGTKVEIKRT		

FIG. 2

Maytansinoids
(DM1)

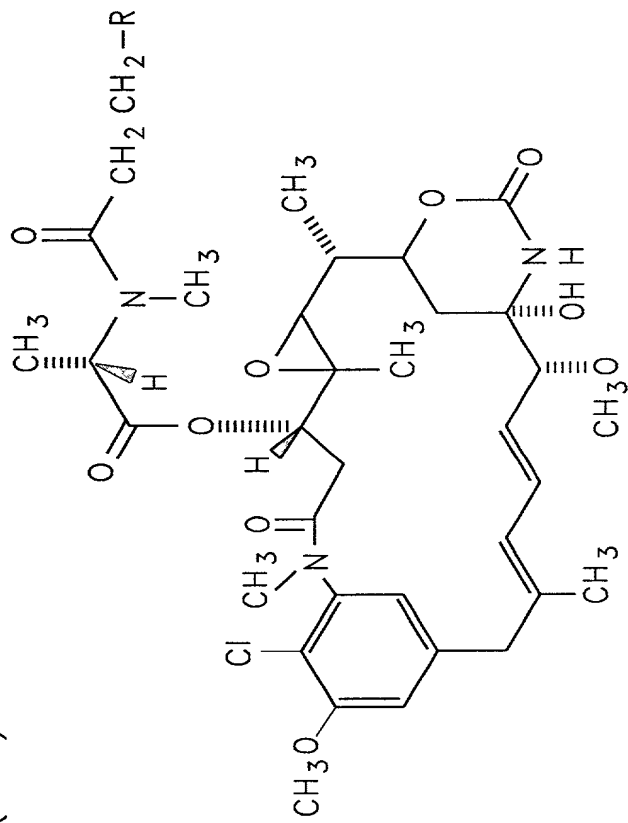


FIG. 3

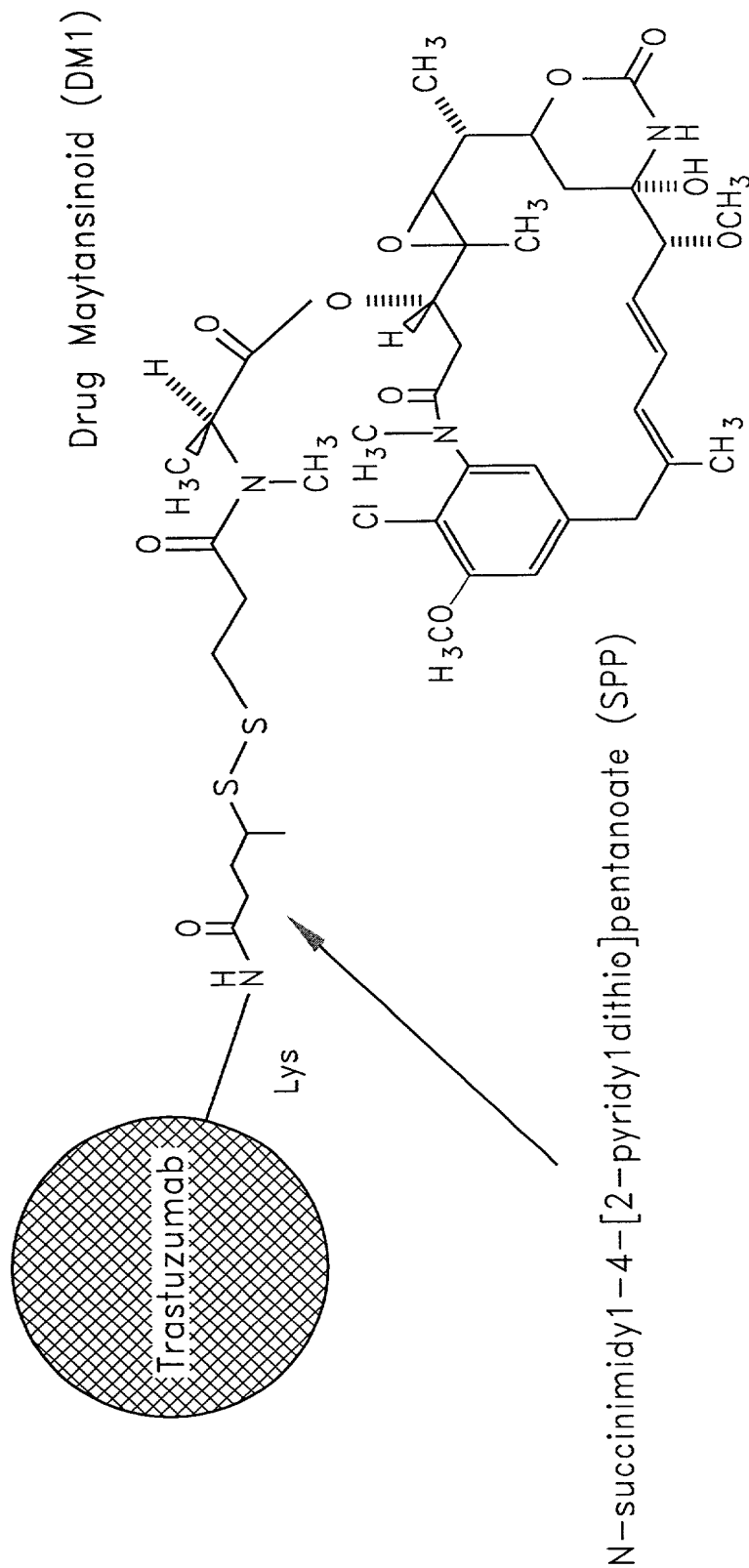


FIG. 4

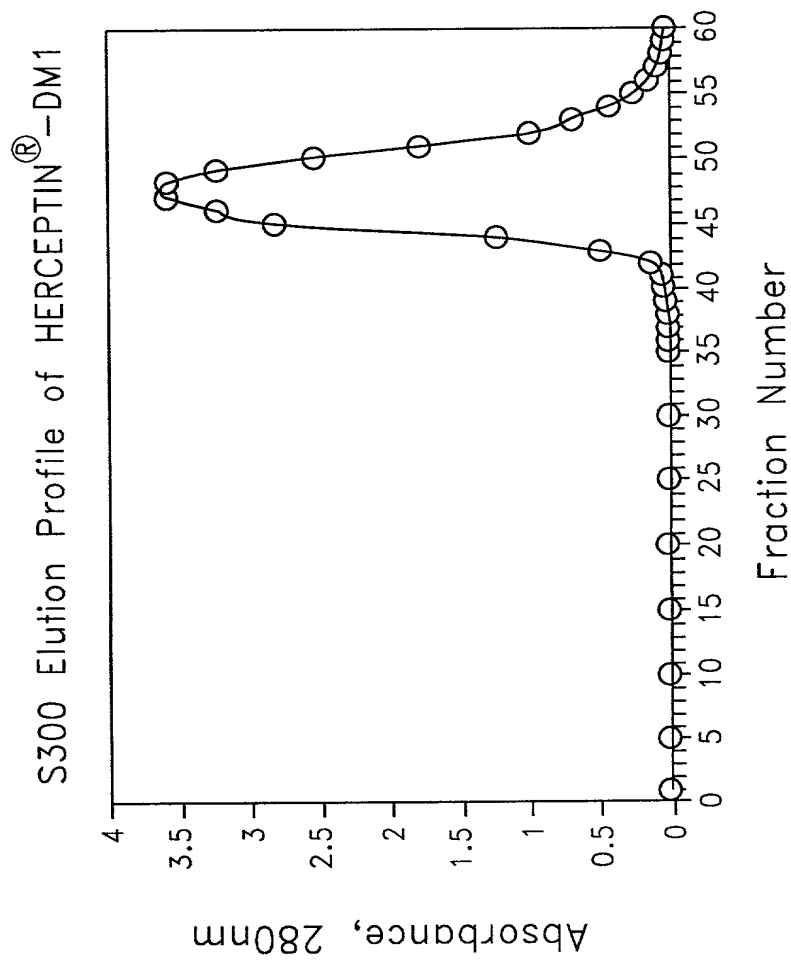


FIG. 5

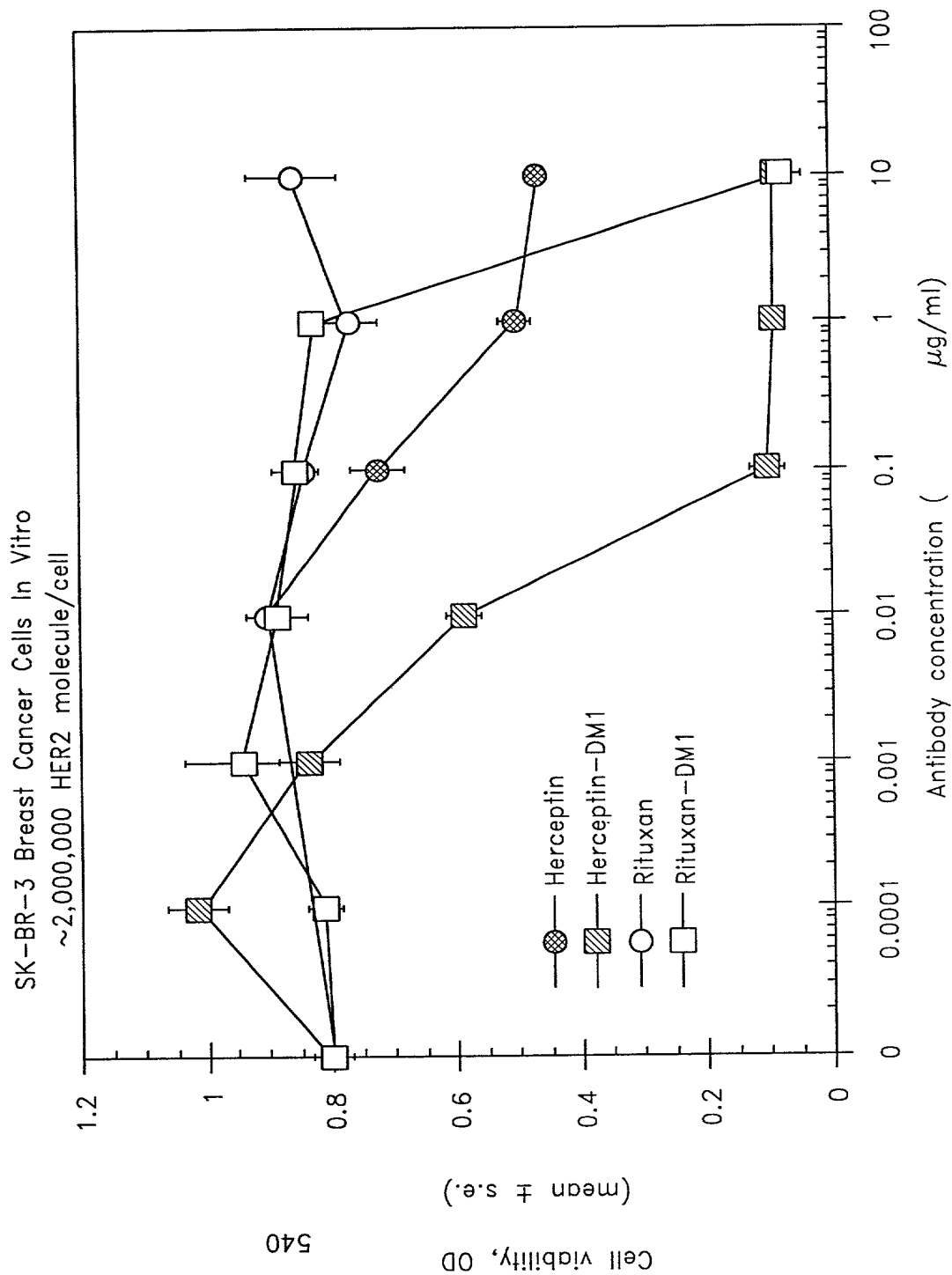


FIG. 6

[illegible]

FIG. 7B


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                bsmAI
                esp3I
                foki bsmBI bsrBI tsp45I
                bstF5I aciI maeIII
201 AAGATATATAA AGAGTGCTGA TTTTGTGAGT AAACCTGCAA CAGTCCTAAC ATTACACCTCT TGTGTGTTTG TGTCTGTTCG CCATCCCGTC TCCGCTCGTC
TTCATATATT TCTCACGACT AAAAACTCA TTGAACGTT GTCAGGATTG TAAGTGAGA ACACACAAAC ACAGACAAGC GGTAGGGCAG AGCGAGCAG

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                fnu4HI/bsofI
                haeIII/palI
                mcrI
                eagI/xmaIII/ecI XI
                eaeI
                notI
                fnu4HI/bsofI scfI
                cac8I cfrI tru9I
                pstI
                aluI aciI aciI
                hindIII bsiEI mselI bsgI
301 ACTTATCCTT CACTTTCCAG AGGGTCCCC CGCAGACCCC GGATCGCTAG CTCGGCAATC GATAAGCTTG CGCCCGCTTA ACTGCAGAAG TTGGTCGTGA
TGAATAGGAA GTGAAAGGTC TCCAGGGGG GCGTCTGGG CCTAGCGATC GAGCGCTTAG CTATTGAAAC GCCGGCGAAT TGACGTCTTC AACCAAGCACT
                ^start of BS intron insert at Cla
                ^bp820 in pCI
                ^start of BS insert at HindIII

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```

                pleI
                hinfi
                mboII
                bpuAI
                bbsI
                bsmAI
                taqI
                bsrI
                bsal
                tru9I bsmAI
                mselI bsal
                maeIII
                tspRI bspMI
401 GGCACCTGGC AGGTAAGTAT CAAGGTACA AGACAGGTTT AAGGAGACCA ATAGAACTG GGCTTGTGCA GACAGAGAAG ACTCTGCGT TTCTGATAGG
CCGTGACCG TCCATTCTATA GTTCCAATGT TCTGTCCAAA TTCTCTGCTGATCTTGAC CCGAACAGCT CTGTCTCTTC TGAGAAGCA AAGACTATCC
                ^start of chimeric intron at pCI 857

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FIG. 7D

501

```
CACCTATTGG TCTTACTGAC ATCCACTTTG CCTTCTCTC CACAGGTGTC CACTCCCAGG TTCAATTACA GCTCTTAAGC GGCCGCAAGC TTGATATCGA
GTGGATAACC AGAATGACTG TAGGTGAAC GGAAGAGAG GTGTCCACAG GTGAGGTCC AAGTTAATGT CGAGAAATCG CCGCGTTTCG AACTATAGCT
^end of chimeric intron at pCI 989
end of BS insert at HindIII^
```

```

        hinPI
        hhaI/cfoI
        thaI
        fnuDII/mvnI
        bstUI
        bshI236I
        mwoI sau96I
        hinPI mspI
        hhaI/cfoI
        cac8I hpaII
        bssHII nlaIV
        thaI scrFI
        fnuDII/mvnI
        mnlI bstUI nciI
        xhoI bshI236I haeIII/paI
        smlI hinPI dsav
        paer7I hhaI/cfoI asuI
        aluI avaI cac8I cauII
        hindIII taqI bssHII bssKI
        TTCGAGGG CGCGGCGCGG GCCCCACCC CTCGCAGCAC CCCGCGCCCC
        AAGTTTTCG AAGTTTTCG CGCGGCGGCG CGGGGCTGTG GGGCGCGGGG
        ^end of BS intron insert at spe
        ^start of human HER2 from BS at xhol

```


bstEII
 scrFI
 mvaI
 ecorII
 dsav
 bstNI
 bstKI hphI
 apyI tsp45I
 tseI
 fnu4HI/bsoFI
 bbvI
 aluI tspRI bslI bsaII maeII
 tsPRI sfanI
 GTGAGCTGCA CTGCCAGCC CTGGTCACCT ACAACACAGA CACGTTTGAG TCCATGCCCA ATCCCGAGG CGGCGATACA
 GAAGTGGTG TCACCGTAGA CACTCGACGT GACGGGTCGG GACCAGTGGA TGTGTGTCT GTGCAAACTC AGGTACGGGT TAGGGCTCCC GGCCATATGT
 F N H S G I C E L H C P A L V T Y N T D T F E S M P N P E G R Y T
 cac8I
 hinPI
 hhaI/cfoI
 nlaIV
 nari
 kasi
 hinII/acyI
 hgiCI
 haeII aluI
 eheI pvuII
 banI mspAII/nspBII
 ahaII/bsaHI maeII
 bsmFI
 bsmFI
 TACAACTACC TTCTACGGA CGTGGGATCC TGCACCTCG TGTGCCCTCG GCACAACCAA GAGGTGACAG
 TTCGGCGCCA GCTGTGTGAC TGCCTGTCCC TGCCTGTGAC TGCCTGTGAC TGCCTGTGAC TGCCTGTGAC TGCCTGTGAC
 AACCCGGGT CGACACACTG ACGGACAGG ATGTTGATGG AAAGATGCCT GCACCTAGG ACGTGGAGC AGAGGGGGA CGTGTGGTT CTCACACTGC
 F G A S C V T A C P Y N Y L S T D V G S C T L V C P L H N Q E V T A
 ahdI/eam1105I
 tsp45I
 mspAII/nspBII
 ahaII/bsaHI maeII
 bsmFI
 bsmFI
 TACAACTACC TTCTACGGA CGTGGGATCC TGCACCTCG TGTGCCCTCG GCACAACCAA GAGGTGACAG
 TTCGGCGCCA GCTGTGTGAC TGCCTGTCCC TGCCTGTGAC TGCCTGTGAC TGCCTGTGAC TGCCTGTGAC TGCCTGTGAC
 AACCCGGGT CGACACACTG ACGGACAGG ATGTTGATGG AAAGATGCCT GCACCTAGG ACGTGGAGC AGAGGGGGA CGTGTGGTT CTCACACTGC
 F G A S C V T A C P Y N Y L S T D V G S C T L V C P L H N Q E V T A
 cac8I
 tseI
 fnu4HI/bsoFI
 bbvI
 aluI tspRI bslI bsaII maeII
 tsPRI sfanI
 GTGAGCTGCA CTGCCAGCC CTGGTCACCT ACAACACAGA CACGTTTGAG TCCATGCCCA ATCCCGAGG CGGCGATACA
 GAAGTGGTG TCACCGTAGA CACTCGACGT GACGGGTCGG GACCAGTGGA TGTGTGTCT GTGCAAACTC AGGTACGGGT TAGGGCTCCC GGCCATATGT
 F N H S G I C E L H C P A L V T Y N T D T F E S M P N P E G R Y T
 hgiAI/asphI
 bsp1286
 bsiHKAI
 bmyI
 nlaIII
 hphI
 mnlI mnlI
 bsrI
 maeII
 CGAGAGGTGA GGCAGTTAC
 GCTCTCCACT CCGTCAATG
 E D G T Q R C E K C S K P C A R V C Y G L G M E H L R E V R A V T

FIG. 7I

sau96I
 nlaIV
 avall
 asul
 sandI
 ppumi
 nlaIV
 ecoO109I/draII
 bsmFI
 mnlI
 tspRI
 801 CAGTGCCAAAT ATCCAGGAGT TTGCTGGCTG CAAGAAGATC TTGGGAGCC TGGCATTCTT GCGGAGAGC TTTGATGGGG ACCGAGCCTC CAACACTGCC
 GTCACGGTTA TAGTCTCTCA AACGACCGAC GTTCTTCTAG AACCCCTCGG ACCGTAAGA CGGCCTCTCG AACTACCCG TGGGTGGAG GTTGTGACGG
 358 S A N I Q E F A G C K I F G S L A F L P E S F D G D P A S N T A
 xcmI
 scrFI
 mvaI
 ecoRII
 dsav
 bstNI
 bssKI
 apyI
 cac8I
 mboII
 nlaIV
 mspI
 hpaII
 aluI
 801 CAGTGCCAAAT ATCCAGGAGT TTGCTGGCTG CAAGAAGATC TTGGGAGCC TGGCATTCTT GCGGAGAGC TTTGATGGGG ACCGAGCCTC CAACACTGCC
 GTCACGGTTA TAGTCTCTCA AACGACCGAC GTTCTTCTAG AACCCCTCGG ACCGTAAGA CGGCCTCTCG AACTACCCG TGGGTGGAG GTTGTGACGG
 358 S A N I Q E F A G C K I F G S L A F L P E S F D G D P A S N T A
 bpmI/gsuI
 tseI
 fnu4HI/bsoFI
 bbsKI
 apyI
 cac8I
 mboII
 nlaIV
 mspI
 hpaII
 aluI
 801 CAGTGCCAAAT ATCCAGGAGT TTGCTGGCTG CAAGAAGATC TTGGGAGCC TGGCATTCTT GCGGAGAGC TTTGATGGGG ACCGAGCCTC CAACACTGCC
 GTCACGGTTA TAGTCTCTCA AACGACCGAC GTTCTTCTAG AACCCCTCGG ACCGTAAGA CGGCCTCTCG AACTACCCG TGGGTGGAG GTTGTGACGG
 358 S A N I Q E F A G C K I F G S L A F L P E S F D G D P A S N T A
 bsrBI
 aciI
 mwol
 bbsKI
 apyI
 cac8I
 mboII
 nlaIV
 mspI
 hpaII
 aluI
 801 CAGTGCCAAAT ATCCAGGAGT TTGCTGGCTG CAAGAAGATC TTGGGAGCC TGGCATTCTT GCGGAGAGC TTTGATGGGG ACCGAGCCTC CAACACTGCC
 GTCACGGTTA TAGTCTCTCA AACGACCGAC GTTCTTCTAG AACCCCTCGG ACCGTAAGA CGGCCTCTCG AACTACCCG TGGGTGGAG GTTGTGACGG
 358 S A N I Q E F A G C K I F G S L A F L P E S F D G D P A S N T A
 901 CCGCTCCAGC CAGAGCAGCT CCAAGTGTTT GAGACTCTGG AAGAGATCAC AGGTTACCTA TACATCTCAG CATGGCCGGA CAGCCTGCCT GACCTCAGCG
 GCGGAGTCTG GTCTGCTCGA GGTTCACAAA CTCTGAGACC TTCTCTAGTG TCCAATGGAT ATGTAGAGTC GTACCGGCT GTGGAGTCCG
 391 P L Q P E Q L Q V F E T L E E I T G Y L Y I S A W P D S L P D L S V
 hinPI
 hhaI/cfoI
 nlaIV
 nari
 kasi
 hinII/acyI
 hgiCI
 haeII
 eheI
 banI
 ahaII/bsaHI mwol
 bsII
 001 TCTTCCAGAA CCTGCAAGTA ATCCGGGAC GAATTCTGCA CAATGGGCGC TACTCGCTGA CCCTGCAAGG GCTGGGCATC AGCTGGCTGG GGCTGGCTC
 AGAAGGTCTT GGAGTTCAT TAGGCCCTG CTTAAGACGT GTTACCGCGG ATGAGCGACT GGGACGTTCC CGACCCGTAG TCGACCGACC CCGACCGGAG
 425 F Q N L Q V I R G R I L H N G A Y S L T L Q G L G I S W L G L R S
 alwNI
 alw26I/bsmAI
 bsmFI
 scrFI
 nciI
 mspI
 hpaII
 dsav
 caulI
 bssKI
 bsaJI
 apoI
 001 TCTTCCAGAA CCTGCAAGTA ATCCGGGAC GAATTCTGCA CAATGGGCGC TACTCGCTGA CCCTGCAAGG GCTGGGCATC AGCTGGCTGG GGCTGGCTC
 AGAAGGTCTT GGAGTTCAT TAGGCCCTG CTTAAGACGT GTTACCGCGG ATGAGCGACT GGGACGTTCC CGACCCGTAG TCGACCGACC CCGACCGGAG
 425 F Q N L Q V I R G R I L H N G A Y S L T L Q G L G I S W L G L R S
 hinPI
 hhaI/cfoI
 pvuII
 mspAI/nsbII
 fnu4HI/bsoFI
 sfaNI
 aluI
 mwol
 bbsKI
 apyI
 cac8I
 hinPI
 hhaI/cfoI
 tseI
 001 TCTTCCAGAA CCTGCAAGTA ATCCGGGAC GAATTCTGCA CAATGGGCGC TACTCGCTGA CCCTGCAAGG GCTGGGCATC AGCTGGCTGG GGCTGGCTC
 AGAAGGTCTT GGAGTTCAT TAGGCCCTG CTTAAGACGT GTTACCGCGG ATGAGCGACT GGGACGTTCC CGACCCGTAG TCGACCGACC CCGACCGGAG
 425 F Q N L Q V I R G R I L H N G A Y S L T L Q G L G I S W L G L R S

FIG. 7J

[illegible]

FIG. 7M

[illegible]

FIG. 7N

[illegible]

FIG. 70

Year	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

1

rmaI
 maeI
 styI
 bsaJI
 bliI
 avrII
 haeIII/pal
 stuI
 haeI
 mnlI bfaI
 TTTGGAGGCC
 AACCTCCGG

mnlI aluI
 haeIII/palI
 fnu4HI/bsoFI
 aciI ddeI
 CGCGCGGAGA CTCGATAAGG TCTTCATCAC TCCTCCGAAA AACCTCCGG

sau96I
 sau96I
 pspOMI/bsp120I
 nlaIV
 hgiJII
 thai haeIII/palI
 fnuDII/mvNI
 sacII/sstII
 mspAII/nspBII
 kspI bsp1286
 dsal bmyI
 bsaJI asuI
 fnu4HI/bsoFI
 haeIII/palI
 mcrI banII
 eagI/smaIII/eclXI
 eaeI cac8I
 cfrI aciI
 bsiEI asuI
 notI bstUI
 fnu4HI/bsoFI
 aciI bshI236I
 bsrBI aciI apaI
 GAGCGGCCGC GGGCCCATCG CCTCTGACAG CAACGTCTAT GACCTCCTAA
 CTGAGACTGTC GTTCAGATA CTGGAGGATT
 ^start of hgh ex 4 (cla/nar)

ddeI
 mnlI
 eco8II
 mwoI
 bsu36I/mstII/sauI
 TGTCCTCAGG GAGCAGGGAA
 CAGCGGTCT TCGGACTAC ACAGGAGTCC CTCGTCCCTT

mwOI
 haeIII/palI
 haeI
 aciI
 CAGAAAGCCA AGTCGCGAGA AGCCCTGATG
 GTCTCCGGT TCAGCGTCT

xhoI
 smlI
 pleI
 taqI taqI
 salI paeR7I
 claI/bsp106 hinfI
 aluI bspDI
 hindIII taqI
 accI avaI
 scaI xbaI
 csp6I bfaI
 rmaI maeI
 fnu4HI/bsoFI
 aciI bshI236I
 bsrBI aciI apaI
 GAGCGGCCGC GGGCCCATCG CCTCTGACAG CAACGTCTAT GACCTCCTAA
 CTGAGACTGTC GTTCAGATA CTGGAGGATT
 ^start of BS insert of HER2 xba-hindIII
 ^end of human HER2 insert from BS at xhoI

mnlI
 ecoNI
 bslI
 tail
 maeII
 mnlI dtdI
 CAACGTCTAT GACCTCCTAA
 CTGAGACTGTC GTTCAGATA CTGGAGGATT
 ^start of hgh ex 4 (cla/nar)

^TG PCR 5' pri

FIG. 7U

```

rmaI      mspI
maeI      hpaII
bfai      scrFI
sau96I    nciI
avaII     dsav
asuI      cauII
          bssKI
          bslI
          tseI bslI
          fnu4HI/bsoFI
          mnlI mboII bsaJI bsrI bglII scfI taqI
          ppuMI mnlI          bstFI          scfI          taqI
          eco0109I/draII sfaNI          mnlI mboII bsaJI bsrI bglII scfI          taqI
701 AGGACCTAGA GGAAGGCATC CAAACGCTGA TGGGGAGGCT GGAAGATGGC AGCCCCCGGA CTGGGCAGAT CTTCAAGCAG ACCTACAGCA AGTTCGACAC
    TCCTGGATCT CCTTCCGTAG GTTGGCGACT ACCCTCCGA CCTTCTACCG TCGGGGGGCT GACCCGTCTA GAAGTTCGTC TGGATGTCGT TCAAGCTGTG
    ^end of ex 4/ start ex 5

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801 AAACACAC AACGATGAC CACTACTCAA GAACTACGGG CTGCTCTACT GCTTCAGGAA GGACATGGAC AAGGTCGAGA CATTCTCTGG CATCGTGCAG
    TTTGAGTGTG TTGCTACTGC GTGATGAGTT CTTGATGCCC GACGAGATGA CGAAGTCCTT CCTGTACCTG TTCCAGCTCT GTAGGACGC GTAGCAGTC

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FIG. 7V

scrFI mwoI
 mvaI thaI
 ecorII fnuDI/mvni
 dsav bstUI
 bstNI bsh1236I
 bssKI
 bsII bslI
 cac8I apyI bslI
 haeIII/palI HaeIII/palI fnu4HI/bsoFI
 haeI haeI nlaIV haeIII/palI
 901 CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG GCACGCAAAA GGCAGGAAC CGTAAAAAGG CGCGTTGCT
 GCCATTATGC CAATAGGTGT CTTAGTCCCC TATTGCGTCC TTTCTTGATC ACTCGTTTC CGGTCGTTTT CGGTCCTTG GCATTTTCC GCGCAACGA
 nlaIII nspHI
 nspI nspI
 aflIII
 tfII
 hinFI
 aciI
 nlaIV
 001 GGCGTTTTC CATAGGCTCC GCCCCCTGA CGAGCATCAC AAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCGACAC GACTATAAAG ATACCAGGCG
 CCGCAAAAAG GTATCCGAGG CGGGGGGACT GCTCGTAGTG TTTTGTAGCTG CGAGTTGAGT CTCACCGCT TTGGGCTGTC CTGATATTTC TAATGTCGCG
 hgaI
 drdI
 taqI smlI mnlI
 bciVI
 mspi
 hpaII
 bslI hpaII
 aciI bsaWI
 fnu4HI/bsoFI
 bssSI hinPI
 hhaI/cfoI
 101 TTTCCCCCTG GAAGTCCCT CGTGGCTCT CCTGTTCGGA CCTGCGCTTACCGGATAC CTGTCCGCTT TTCTCCTTC GGAAGCGTG CGGCTTCTC
 AAAGGGGAC CTTGAGGGA GCACGCGAGA GGAACAAGCT GGGACGCGGA ATGGCTATG GACAGGCGGA AAGAGGAAG CCCTTCGCAC CGCAAAAGAG
 hgiAI/aspHI
 bsp1286
 bsiHKAI
 bmyI
 apaLI/snoI
 alw44I/snoI
 tseI
 fnu4HI/bsoFI
 mspALI/nspBII mspi
 aciI hinPI hpaII
 mcrI bbvI bsaWI
 bsiEI hhaI/cfoI
 201 AATGCTCACG CTGTAGGTAT CTCAGTTCCG TGTAGGTCGT TCGCTCCAAG CTGGGCTG TGACGGAACC CCGACCGCT CGGCTTATC
 TTACGAGTGC GACATCCATA GAGTCAAGCC ACATCCAGCA AGCGAGGTC GACCCGACAC ACGTGTCTGG GGGGCAAGTC GGGCTGGCGA CGCGAATAG

FIG. 7AA


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trp9I      nlaIV
tsp509I    hgiCI
trp9I      mnlI
msei msei  trp9I  msei  mnlI  msei  mnlI  msei  mnlI  msei  mnlI
ahaIII/draI  msei  mnlI  msei  mnlI  msei  mnlI  msei  mnlI  msei  mnlI
ahaIII/draI  msei  mnlI  msei  mnlI  msei  mnlI  msei  mnlI  msei  mnlI
701 CTTTAAAT AAAAATGAAG TTTTAAATCA ATCTAAAGTA TATATGAGTA AACCTGGTCT GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG
GAAAATTTAA TTTTACTTTC AAAAATTTAGT TAGATTTCAT ATATACTCAT TTGAACCCAGA CTGTCAATGG TTACGAATTA GTCACTCCGT GGATAGAGTC
801 CGATCTGTCT ATTTCGTCTA TCCATAGTTG CCTGACTCCC CFTGCTGTAG ATAACTACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT
GCTAGACAGA TAAAGCAAGT AGGTATCAAC GGAAGTGGG GGAAGTGGG GGAAGTGGG GGAAGTGGG GGAAGTGGG GGAAGTGGG GGAAGTGGG GGAAGTGGG
901 ACCGCGAGAC CCAGCTCAG CGGCTCCAGA TTTATCAGCA ATAAACCCAG CAGCGGAAG GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCTCC
TGCGGCTCTG GGTGGGAGTG GCCGAGGTCT AAATAGTCTT TATTGGTCTG GTCCGCTTC GTCCGCTTC GTCCGCTTC GTCCGCTTC GTCCGCTTC GTCCGCTTC
001 ATCCAGTCTA TTAATGTGTG CCGGGAAGCT AGAGTAAGTA GTTGGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC TGCTGGCATC GTGGTGTCTAC
TAGGTCAGAT AATTAACAAC GGCCCTTCGA TCTCATTCAT CAAGCGGTCA ATTATCAAC GGGTTGCAAC AACGGTAACG ACGACCGTAG CACCACAGTG

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FIG. 7CC

[illegible]

FIG. 7DD

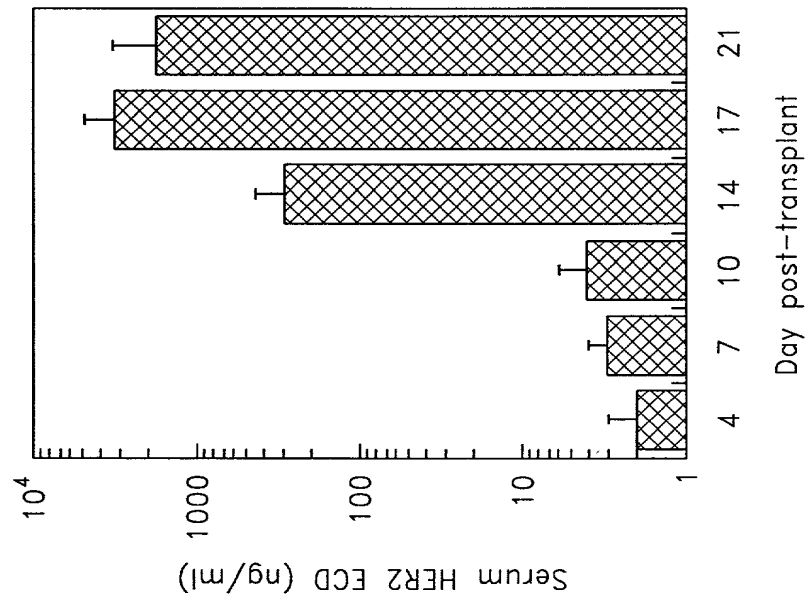


FIG. 8A

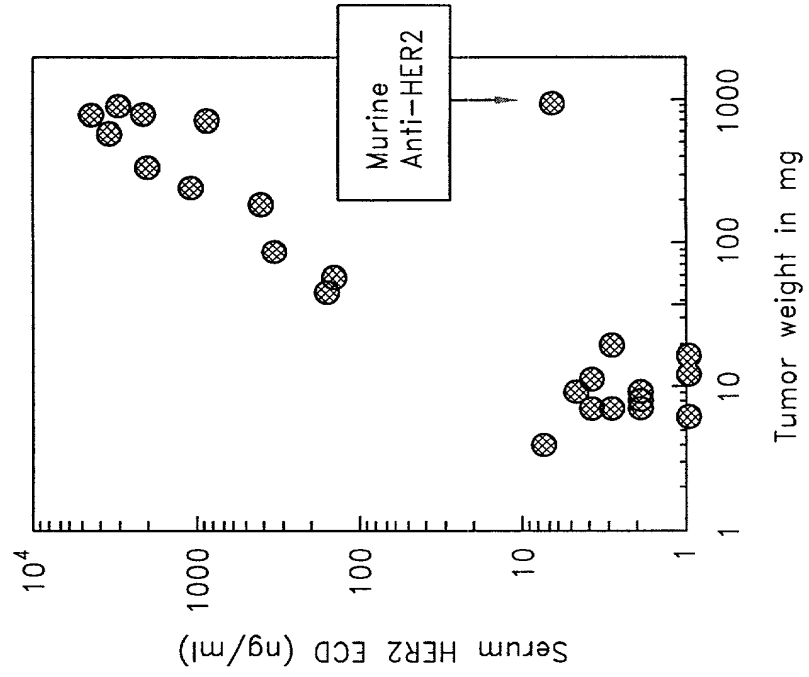


FIG. 8B

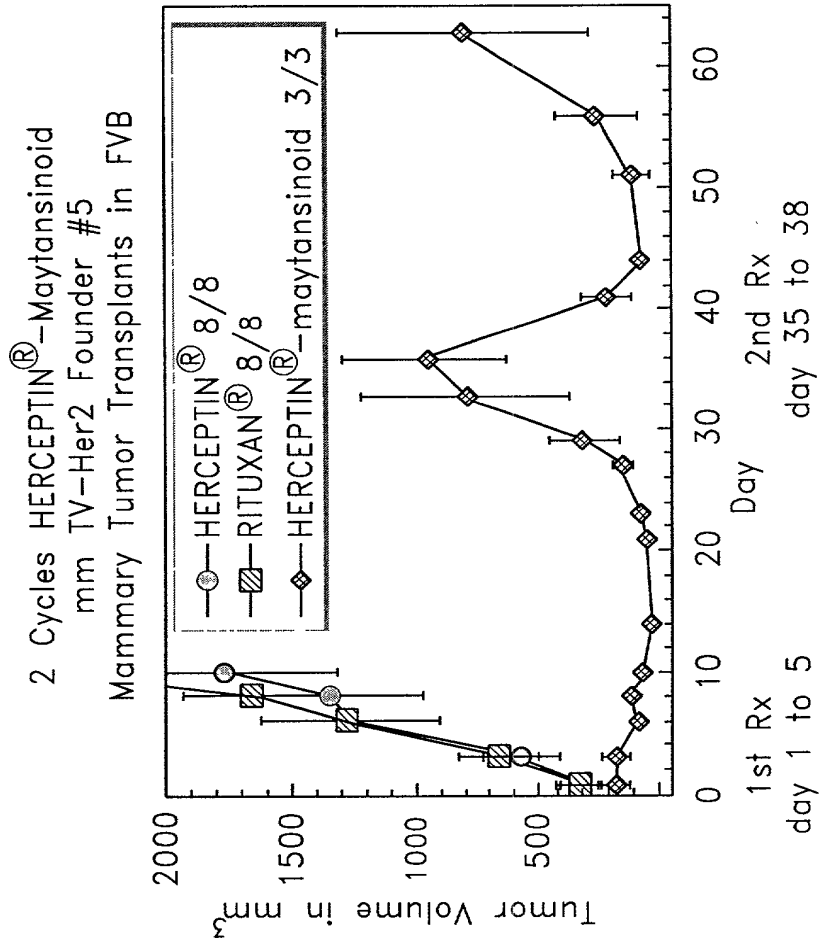


FIG. 9

HER2 Y.P. C-2 Herceptin Both

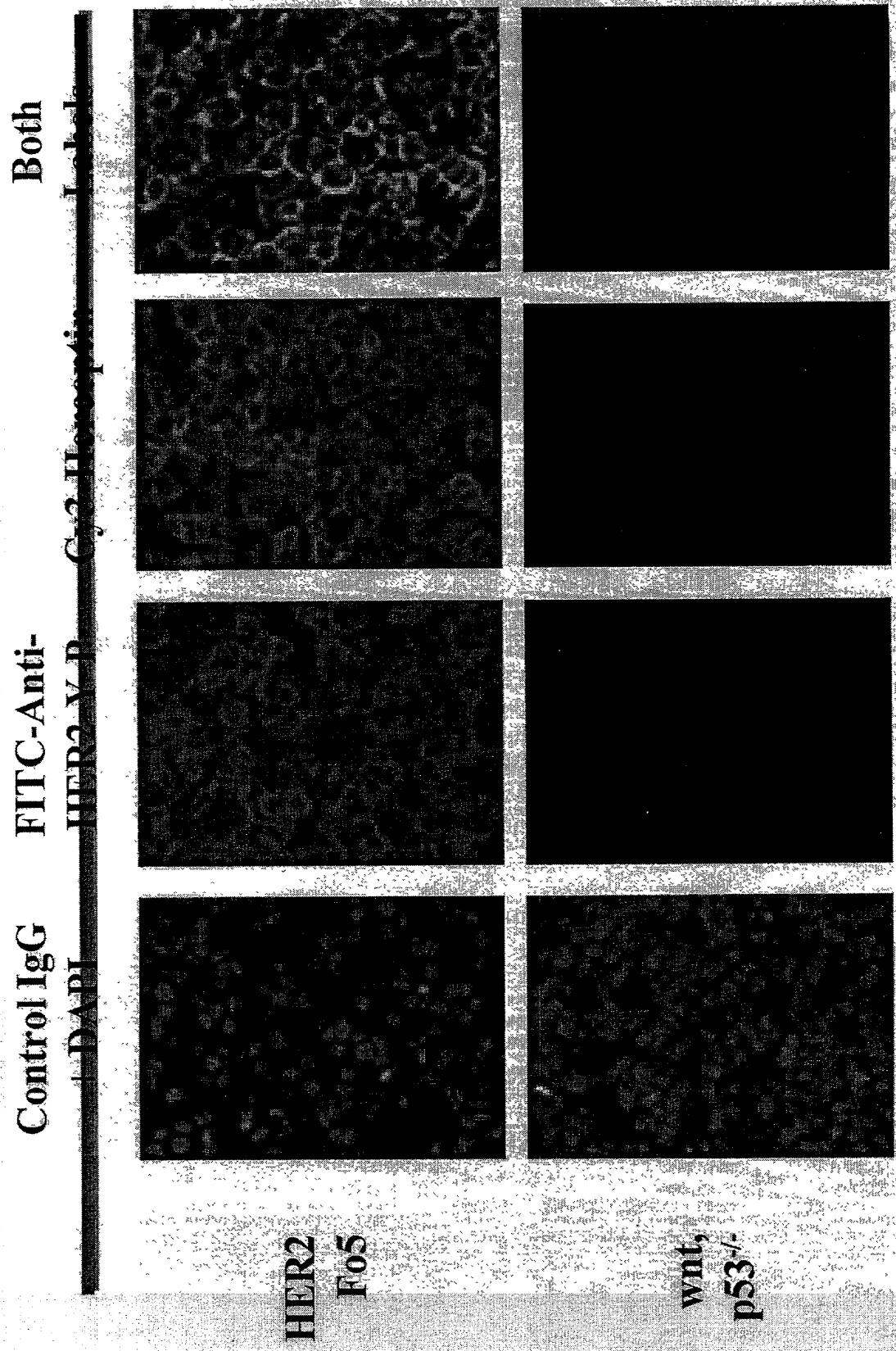


FIG. 10

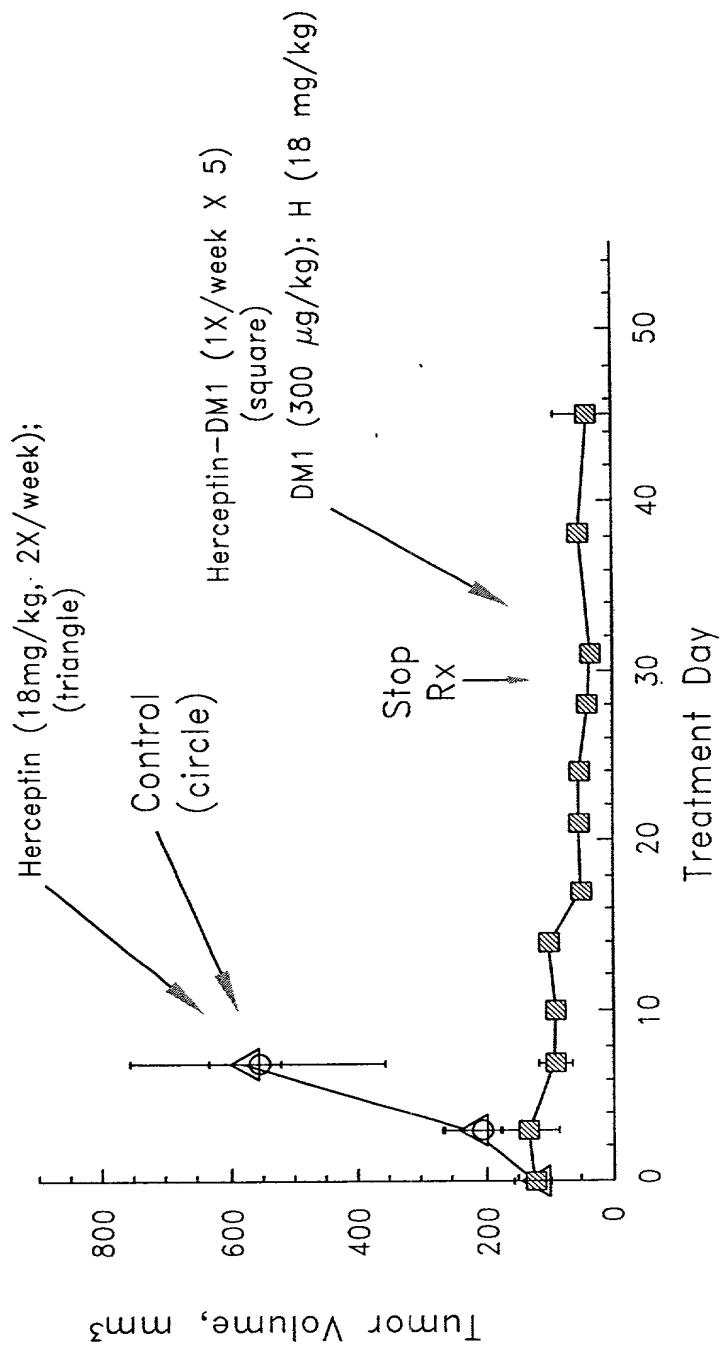


FIG. 11

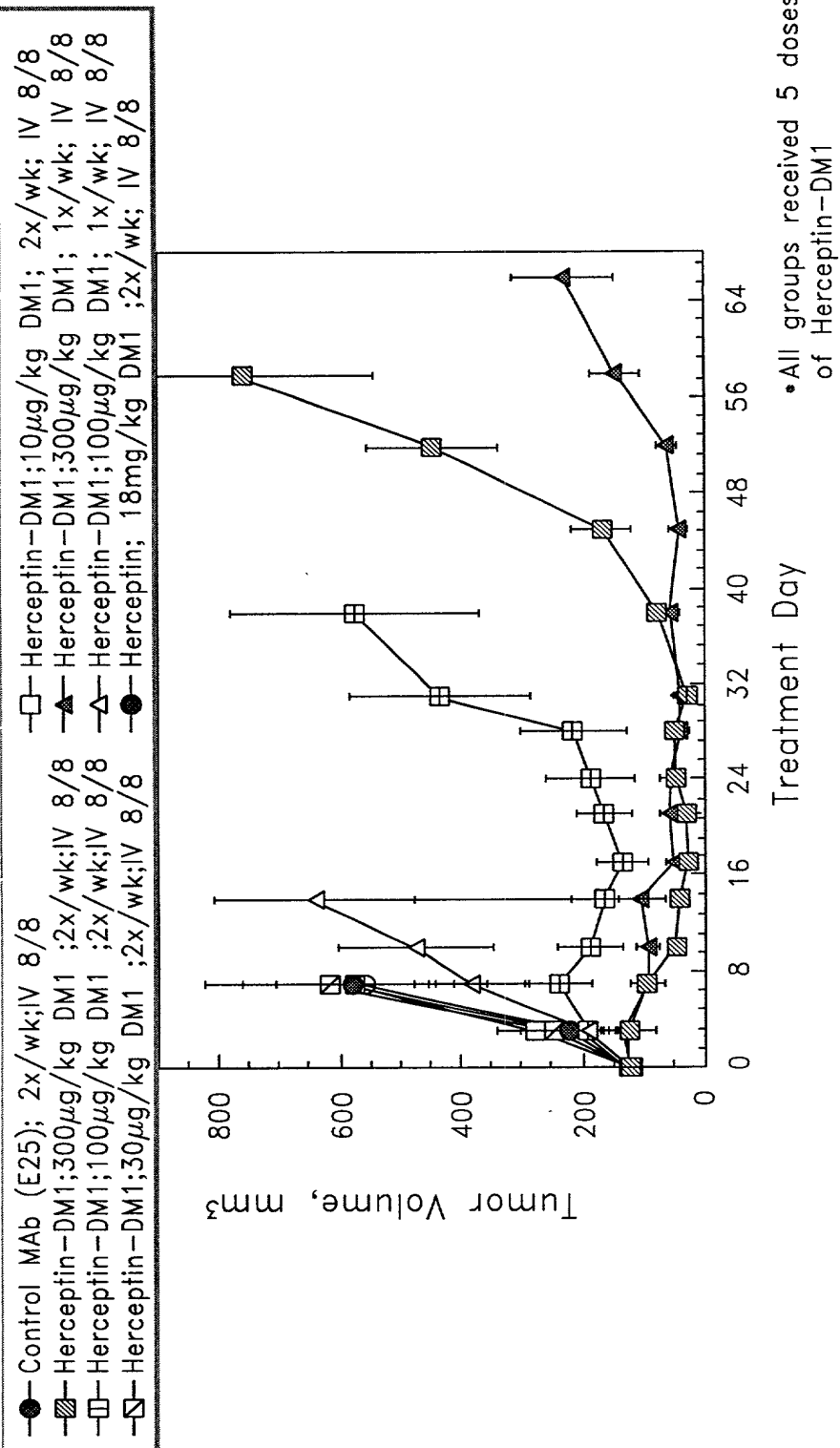


FIG. 12

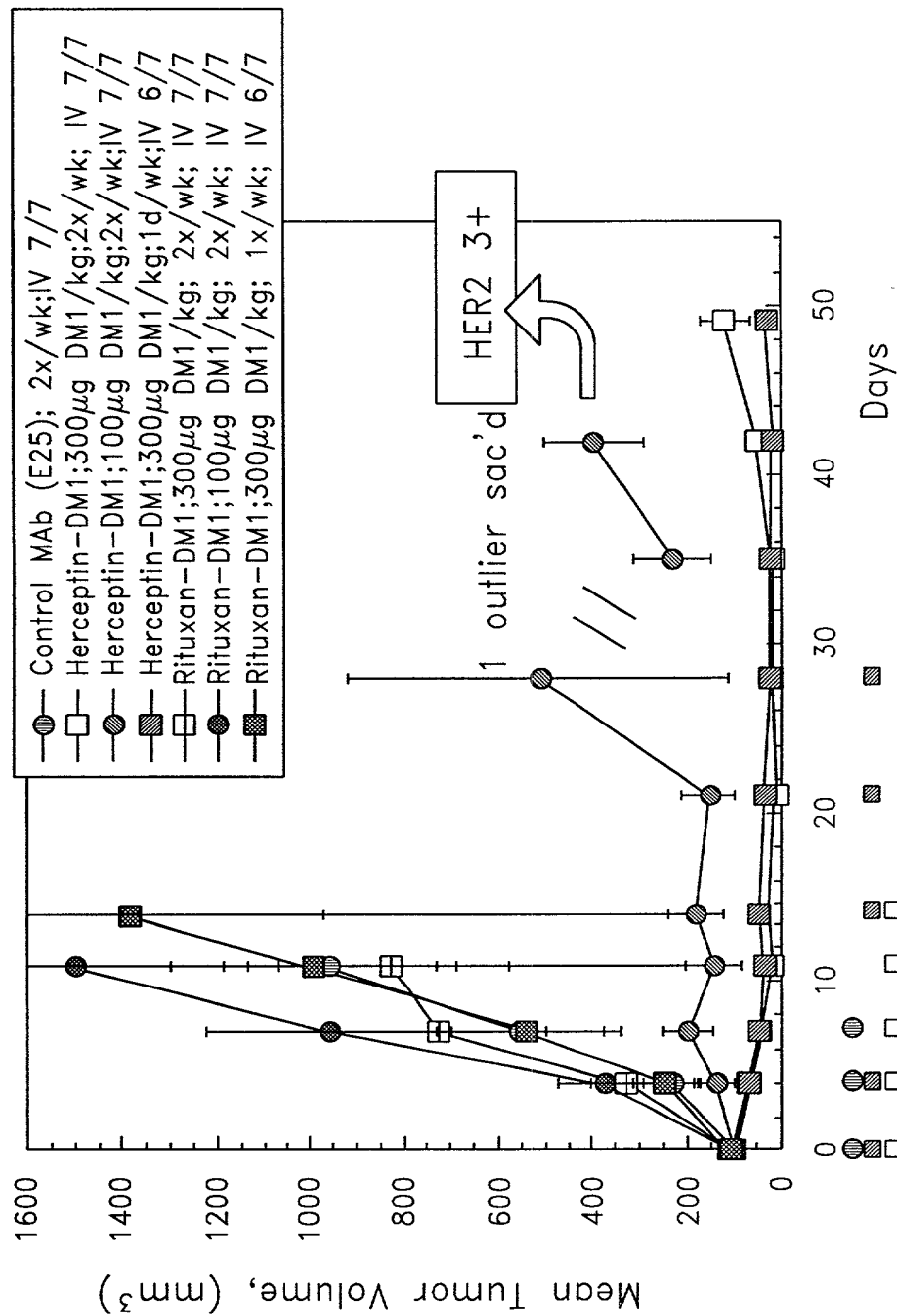


FIG. 13

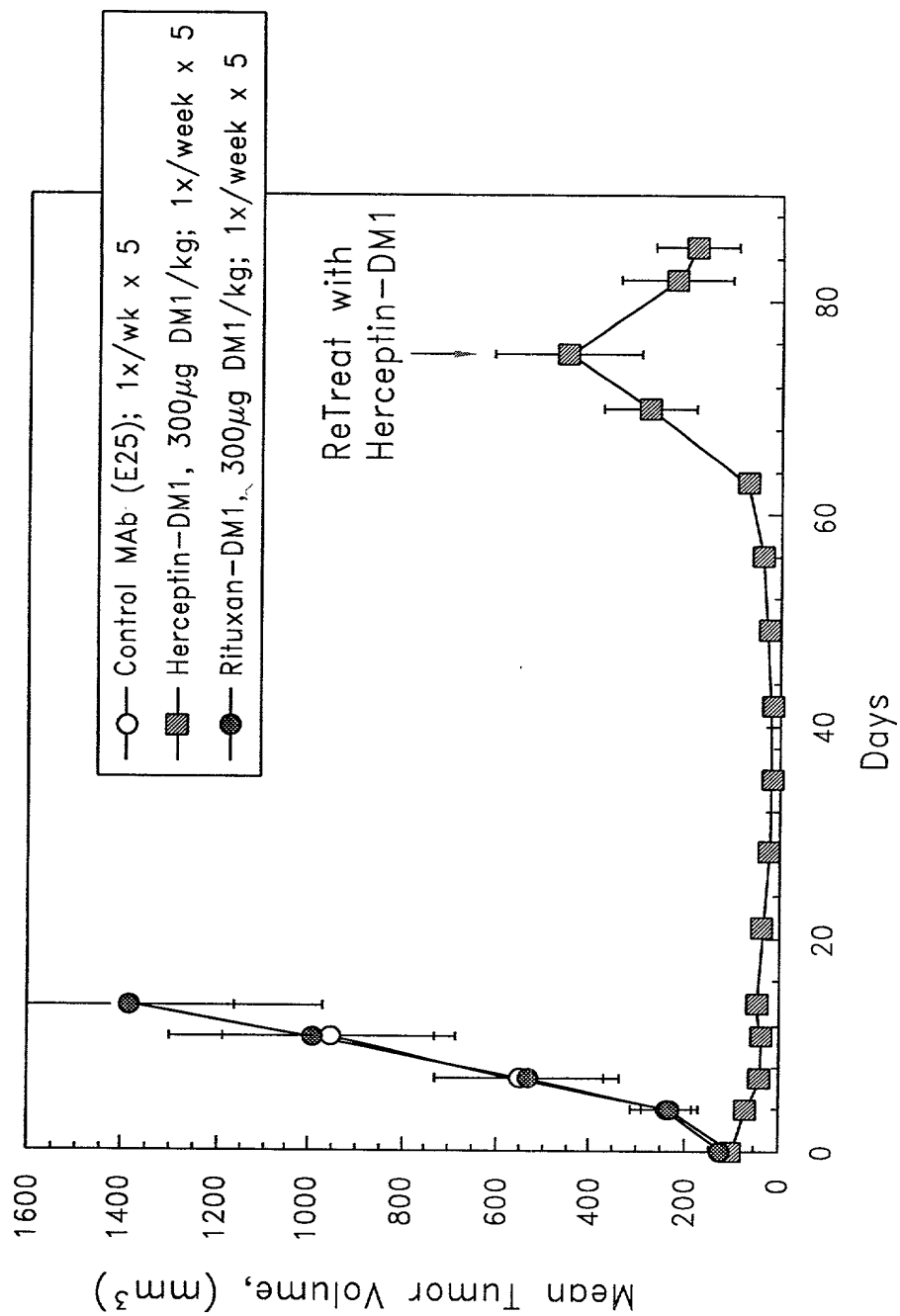


FIG. 14